

This Page Is Inserted by IFW Operations  
and is not a part of the Official Record

## **BEST AVAILABLE IMAGES**

Defective images within this document are accurate representations of the original documents submitted by the applicant.

Defects in the images may include (but are not limited to):

- BLACK BORDERS
- TEXT CUT OFF AT TOP, BOTTOM OR SIDES
- FADED TEXT
- ILLEGIBLE TEXT
- SKEWED/SLANTED IMAGES
- COLORED PHOTOS
- BLACK OR VERY BLACK AND WHITE DARK PHOTOS
- GRAY SCALE DOCUMENTS

**IMAGES ARE BEST AVAILABLE COPY.**

**As rescanning documents *will not* correct images,  
please do not report the images to the  
Image Problem Mailbox.**

## Sequence Comparison A

```

RESULT 1
US-08-253-155A-12
; Sequence 12, Application US/08253155A
; Patent No. 5691147
; GENERAL INFORMATION:
;   APPLICANT: Gyuris, Jeno
;   APPLICANT: Draetta, Giulio
;   TITLE OF INVENTION: CDK4 Binding Proteins
;   NUMBER OF SEQUENCES: 95
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: LAHIVE & COCKFIELD
;     STREET: 60 State Street
;     CITY: Boston
;     STATE: MA
;     COUNTRY: USA
;     ZIP: 02109
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: ASCII(text)
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/08/253,155A
;     FILING DATE: 02-JUN-1994
;     CLASSIFICATION: 435
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Vincent, Matthew P.
;     REGISTRATION NUMBER: 36,709
;     REFERENCE/DOCKET NUMBER: MII-028
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: (617) 227-7400
;     TELEFAX: (617) 227-5941
;   INFORMATION FOR SEQ ID NO: 12:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH: 1075 base pairs
;       TYPE: nucleic acid
;       STRANDEDNESS: single
;       TOPOLOGY: linear
;     MOLECULE TYPE: cDNA
US-08-253-155A-12

```

```

Query Match          21.6%; Score 890; DB 1; Length 1075;
Best Local Similarity 96.2%; Pred. No. 2.1e-237;
Matches 975; Conservative 1; Mismatches 31; Indels 7; Gaps 6;

```

```

Qy  2918 tcaccatcttcggccctgtcaacaacagcaccatgaaaatcgaccactttcagctagata 2977
      || || |||||
Db   44 TCTGCAAGTTTCGGCCCTGTCAACAACAGCACCATGAAAATCGACCACCTTTCAGCTAGATA 103

Qy  2978 atgagaagcccatgcgagtgggtgatgatgaagacttggttagaccagcgctctcatcagcg 3037
      |||||
Db   104 ATGAGAAGCCCATGCGAGTGGTGGATGATGAAGACTGGGTAGACCAGCGTCTCATCAGCG 163

Qy  3038 agctgaggaaagagtacggaatgacctacaatgacttcttcatggtgctaacagatgtgg 3097
      |||||
Db   164 AGCTGAGGAAGGAGTACGGATTGACCTACACTGA-TTCTTCATGGTGCTAACAGATGTGG 222

Qy  3098 atctgagagtcaagcaatactatgaggtaccaataacaatgaagtctgtgtttg-atctg 3156
      |||||
Db   223 ATCTGAGAGTCAAGCAATACTATGAGGTACCAATAACAATGAAGTCTGTGTTGCATCTG 282

Qy  3157 atcgatactttccagtcgccgaatcaaagatatggagaagcagaagaaggagggcattgtt 3216
      |||||
Db   283 ATCGATACTTTCCAGTCCCGAATCAAAGATATGGAGAAGCAGAAGAAGGAGGGCATTGTT 342

Qy  3217 tgcaaagaggacaaaaagcagtcacctggagaacttcctatccaggttccggtggaggagg 3276
      |||||

```

Db 343 TGCAAAGAGGACAAAAAGCAGTCCCTGGAGAACTTCCTATCCAGGTTCCGGTGGAGGAGG 402  
 Qy 3277 aggttgctggtgatctctgctcctaacgatgaagactgggcctattcacagcagctctct 3336  
 |||||  
 Db 403 AGGTTGCTGGTGATCTCTGCTCCTAACGATGAAGACTGGGCCTATTACAGCAGCTCTCT 462  
 Qy 3337 gccctcagtggtcagggcgtgcaattttggtctgcgccacataaccattctgaagctttta 3396  
 |||||  
 Db 463 GCCCTCAGTGGTCAGGCGTGCAATTTGGGTCTGCGCCACATAACCATTCTGAAGC-TTTA 521  
 Qy 3397 ggcgttgagaggaagtgggggagtggttagaactgttcccaattaatgggagctctggt 3456  
 |||||  
 Db 522 GCGTGGAGAGAGGAAGTTGGGGAGTCTTAGAACTGTTCCCAATTAATGGGAGCTCTGTT 581  
 Qy 3457 gttgagcgagaagacgtaccagcccatttggtgaaagacattcgtaactattttcaagt 3516  
 |||||  
 Db 582 GTTGAGCGAGAAGACGTWCCAGCCATT-TGAAAGACATTGTAATTAATTTCAAGTG 640  
 Qy 3517 agcccgagtagtctctccatgcttctagtcggaagacggaatgtcaaactcctggtat 3576  
 |||||  
 Db 641 AGCCCGAGTACTTCTCCATGCTTCTAGTCGGAAGACGGAATGTCAAATCCTGGTAT 700  
 Qy 3577 ccttccccaatgtggtccatggtgattgtgtacgatttaattgattcgatgcaacttcgg 3636  
 |||||  
 Db 701 CCTTCCCAATGTGGTCCATGGTGATTGTGTACGATTAAATTGATTGATGCAACTTCGG 760  
 Qy 3637 agacaggaaatggcgattcagcagtcactggggatgcgctgcccagaagatgagtatgca 3696  
 |||||  
 Db 761 AGACAGGAAATGGCGATTACAGCAGTCACTGGGGATGCGCTGCCAGAAAGATGAGTATGCA 820  
 Qy 3697 ggctatgggtaccatagttaccaccaaggataaccaggatgggtaccaggatgactaccgt 3756  
 |||||  
 Db 821 GGCTATGGTTACCATAGTTACCACCAAGGATACCAGGATGGTTACCAGGATGACTACCGT 880  
 Qy 3757 catcatgagagtattcaccatggatacccttactgagcagaaatatgtaaccttagactc 3816  
 |||||  
 Db 881 CATCATGAGAGTTATCACCATGGATACCCTTACTGAGCAGAAATATGTAACCTTAGACTC 940  
 Qy 3817 agccagtttcctctgcagctgctaaaaactacatgtggccagctccattcttccacact-g 3875  
 |||||  
 Db 941 A--CCATTTCTCTGCAGCTGCTGGAACACGATTGGCCAGCTCCATTCTTCCACACTGG 998  
 Qy 3876 cgtactacatttcctgcctttttctttcagtgtttttctaagactaaataaata 3929  
 |||||  
 Db 999 GGTACTACATTTCTGGCTTTTCTTTCAAGGGTTTTCTTTAGGACTTAAATA 1052

09823356 Results  
SEQ ID NO: 9

# SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	4966	100.0	950	20	AAV33298	Human membrane spa
2	3878	78.1	783	20	AAV60344	Human normal bladd
3	3017	60.8	594	22	AAM93619	Human polypeptide,
4	2645	53.3	509	22	AAG62173	Human gene 18-enco
5	2645	53.3	509	22	AAB80382	Secreted protein e
6	2619	52.7	505	22	AAB80430	Gene #12 associate
7	2496	50.3	554	22	AAB80407	Secreted protein e
8	1629	32.8	316	21	AAB43502	Human cancer assoc
9	1343.5	27.1	320	18	AAW19990	Type I, p80 IL-1-r
10	1343.5	27.1	320	21	AAB37795	Human interleukin-
11	1276.5	25.7	278	17	AAR90544	pJG4-5-CDK-BP clon
12	929	18.7	188	22	AAB63253	Human breast cance
13	835	16.8	162	22	AAG62214	Human gene 18-enco
14	758	15.3	189	22	ABB03204	Human musculoskele
15	209.5	4.2	1618	13	AAR27205	Human nestin. Hom
16	209.5	4.2	1618	15	AAR60127	Human nestin prote
17	209.5	4.2	1618	22	AAU03898	Nestin polypeptide
18	208	4.2	1289	22	ABB70840	Drosophila melanog
19	205	4.1	819	22	AAG79176	Amino acid sequenc
20	204.5	4.1	2951	22	ABB60291	Drosophila melanog
21	202.5	4.1	829	22	AAG79168	Amino acid sequenc
22	201.5	4.1	783	20	AAW70586	Human SLAP-130. H
23	201.5	4.1	783	22	AAG79167	Amino acid sequenc
24	201	4.0	1098	22	ABG20365	Novel human diagno
25	199.5	4.0	1976	22	ABB69419	Drosophila melanog
26	195.5	3.9	2663	22	AAB98612	Human tumour suppr
27	195	3.9	649	20	AAW67883	Human secreted pro
28	195	3.9	982	12	AAR13320	Murine Natural Kil
29	193	3.9	2441	16	AAR79054	CREB binding prote
30	193	3.9	2441	19	AAW40058	Cellular transcrip
31	193	3.9	2441	21	AAV94252	Mouse nuclear CREB
32	193	3.9	2441	22	ABB44555	Mouse wound healin
33	192	3.9	854	22	AAU30183	Novel human secret
34	191.5	3.9	2665	22	ABB28314	Human peptide #965
35	191.5	3.9	2665	22	ABB33490	Peptide #996 encod
36	191.5	3.9	2665	22	ABB18950	Protein #949 encod
37	191.5	3.9	2665	22	AAM54270	Human brain expres
38	191.5	3.9	2665	22	AAM66665	Human bone marrow
39	191.5	3.9	2665	22	AAM14533	Peptide #967 encod
40	191.5	3.9	2665	22	AAM26950	Peptide #987 encod
41	191.5	3.9	2665	22	AAM02259	Peptide #941 encod
42	191.5	3.9	3266	21	AAB42491	Human ORFX ORF2255
43	191.5	3.9	6815	22	ABB66811	Drosophila melanog
44	190.5	3.8	1183	22	ABB58769	Drosophila melanog
45	189.5	3.8	2519	22	ABG16636	Novel human diagno

## RESULT 9

AAW19990

ID AAW19990 standard; Protein; 320 AA.

XX

AC AAW19990;

XX

DT 27-AUG-1997 (first entry)

XX

DE Type I, p80 IL-1-receptor intracellular domain ligand.

XX

KW IL; interleukin; receptor; ligand; screening assay; inhibitor;

KW IL-1 mediated response; inflammation; inflammatory; antibody;

KW intracellular domain; CANP; calcium activated neutral protease.

XX

OS Homo sapiens.  
 XX  
 PN WO9640907-A1.  
 XX  
 PD 19-DEC-1996.  
 XX  
 PF 06-MAY-1996; 96WO-US06363.  
 XX  
 PR 07-JUN-1995; 95US-0487942.  
 XX  
 PA (GEMY ) GENETICS INST INC.  
 XX  
 PI Graham J, Lin L;  
 XX  
 DR WPI; 1997-052315/05.  
 DR N-PSDB; AAT71217.  
 XX  
 PT Interleukin-1 receptor intracellular ligand proteins and related DNA  
 PT - used to identify inhibitors of the proteins for treatment of  
 PT inflammation  
 XX  
 PS Claim 3; Page 32-33; 54pp; English.  
 XX  
 CC AAW19990 represents a protein that has interleukin-1 receptor (IL-1-R)  
 CC intracellular ligand activity. IL-1-R intracellular ligand proteins  
 CC are used to screen for agents (e.g. antibodies) that are capable of  
 CC inhibiting or blocking the binding of an IL-1-R intracellular ligand  
 CC to the intracellular domain of IL-1-R, i.e. inhibitors of IL-1  
 CC activity. Such agents can be used to treat inflammatory conditions.  
 XX  
 SQ Sequence 320 AA;

Query Match 27.1%; Score 1343.5; DB 18; Length 320;  
 Best Local Similarity 81.4%; Pred. No. 1.6e-87;  
 Matches 267; Conservative 0; Mismatches 0; Indels 61; Gaps 1;

Qy 586 KKGKTEQDGYQKPTNKHFTQSPKKSVDLLGSFEGKRRLLLITAPKAENNMYVQQRDEY 645  
 |||  
 Db 1 kkggkteqdggyqkptnkhftqspkksvadllgsfegkrlllitapkaennmyvqqrdey 60  
 Qy 646 LESFCKMATRKISVITIFGPNVNSTMKIDHFQLDNEKPMRVVDDDLVDQRLISELRKEY 705  
 |||  
 Db 61 lesfckmatrkisvitifgpnvnstmkidhfqldnekpmrvvddedlvdqrliselrkey 120  
 Qy 706 GMTYNDFFMVLTDVDLRVKQYVEVPITMKSVDLIDTFQSRIDMEKQKKEGIVCKEDKK 765  
 |||  
 Db 121 gmtyndffmvltdvdlrvkqyevpitmksvdlidtfqsrikdmekqkkegivck---- 176  
 Qy 766 QSLENFLSRFRWRRRLVISAPNDEDWAYSQQLSALSQACNFGRLRHITILKLLGVGEEV 825  
 |||  
 Db 177 -----eev 179  
 Qy 826 GGVLELFPINGSSVVEREDVPAHLVKDIRNYFQVSPEYFSMLLVGKDGNVKS WYSPMWS 885  
 |||  
 Db 180 ggvlelfpingssvveredvpahlvkdirnyfqvspeyfsmlllvgkdgnvks wypsmpws 239  
 Qy 886 MVIVYDLIDSMQLRRQEMAIQQLGMRC 913  
 |||  
 Db 240 mvivydlidsmqlrrqemaiqqslgmrc 267

RESULT 11  
 AAR90544  
 ID AAR90544 standard; protein; 278 AA.  
 XX  
 AC AAR90544;  
 XX  
 DT 08-AUG-1996 (first entry)  
 XX



## SUMMARIES

Result No.	% Query		Length	DB	ID	Description
	Score	Match				
1	1343.5	27.1	320	1	US-08-726-525-4	Sequence 4, Appli
2	1343.5	27.1	320	2	US-08-487-942-4	Sequence 4, Appli
3	1343.5	27.1	320	2	US-08-726-036A-4	Sequence 4, Appli
4	1343.5	27.1	320	4	US-09-083-516-4	Sequence 4, Appli
5	682	13.7	358	1	US-08-253-155A-36	Sequence 36, Appl
6	209.5	4.2	1618	1	US-07-853-913-4	Sequence 4, Appli
7	193	3.9	2441	1	US-08-194-468-2	Sequence 2, Appli
8	193	3.9	2441	3	US-08-961-739-2	Sequence 2, Appli
9	185.5	3.7	1848	4	US-08-296-791-6	Sequence 6, Appli
10	185.5	3.7	1848	5	PCT-US95-10661A-6	Sequence 6, Appli
11	183	3.7	1315	3	US-08-899-595-3	Sequence 3, Appli
12	180.5	3.6	1248	2	US-09-080-897-2	Sequence 2, Appli
13	180.5	3.6	1248	4	US-09-323-735-2	Sequence 2, Appli
14	174.5	3.5	1185	4	US-09-041-886-23	Sequence 23, Appl
15	164	3.3	1312	4	US-09-041-886-19	Sequence 19, Appl
16	162.5	3.3	442	3	US-08-834-306-52	Sequence 52, Appl
17	162.5	3.3	442	4	US-08-993-674A-52	Sequence 52, Appl
18	161.5	3.3	737	1	US-08-188-582-16	Sequence 16, Appl
19	161.5	3.3	737	1	US-08-646-715-16	Sequence 16, Appl
20	161	3.2	434	1	US-08-097-830E-3	Sequence 3, Appli
21	161	3.2	434	2	US-08-456-112B-3	Sequence 3, Appli
22	159.5	3.2	447	4	US-09-199-637A-351	Sequence 351, App
23	158	3.2	905	2	US-08-574-959A-9	Sequence 9, Appli
24	158	3.2	905	4	US-09-357-014-9	Sequence 9, Ap

## RESULT 1

US-08-726-525-4

; Sequence 4, Application US/08726525

; Patent No. 5789181

; GENERAL INFORMATION:

; APPLICANT: Lin, Lih-Ling

; APPLICANT: Graham, James

; TITLE OF INVENTION: NOVEL INTERLEUKIN-1 RECEPTOR

; TITLE OF INVENTION: INTRACELLULAR LIGAND PROTEINS AND INHIBITORS OF LIGAND

; TITLE OF INVENTION: BINDING

; NUMBER OF SEQUENCES: 7

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: LEGAL AFFAIRS, GENETICS INSTITUTE, INC.

; STREET: 87 CambridgePark Drive

; CITY: Cambridge

; STATE: MA

; COUNTRY: USA

; ZIP: 02140

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/726,525

; FILING DATE: 07-OCT-1996

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/487,942

; FILING DATE: 07-JUN-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: Brown, Scott A.

; REGISTRATION NUMBER: 32,724

; REFERENCE/DOCKET NUMBER: GI5258

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (617) 498-8224

; TELEFAX: (617) 876-5851

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 320 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-726-525-4

Query Match 27.1%; Score 1343.5; DB 1; Length 320;  
Best Local Similarity 81.4%; Pred. No. 3.1e-90;  
Matches 267; Conservative 0; Mismatches 0; Indels 61; Gaps 1;

Qy 586 KKGKTEQDGYQKPTNKHFTQSPKKSADLLGSFEGKRRLLLITAPKAENNMVQQRDEY 645  
|||||  
Db 1 KKGKTEQDGYQKPTNKHFTQSPKKSADLLGSFEGKRRLLLITAPKAENNMVQQRDEY 60  
  
Qy 646 LESFCKMATRKISVITIFGPVNNSTMKIDHFQLDNEKPMRVVDEDLVDQRLISELRKEY 705  
|||||  
Db 61 LESFCKMATRKISVITIFGPVNNSTMKIDHFQLDNEKPMRVVDEDLVDQRLISELRKEY 120  
  
Qy 706 GMTYNDFFMVLTDVDLRVKQYYEVPITMKSVDLIDTFQSRIKMEKQKKEGIVCKEDKK 765  
|||||  
Db 121 GMTYNDFFMVLTDVDLRVKQYYEVPITMKSVDLIDTFQSRIKMEKQKKEGIVCK---- 176  
  
Qy 766 QSLFNLSRFRWRRRLVISAPNDEDWAYSQQLSALSGQACNFLRHITILKLLGVGEEV 825  
|||  
Db 177 -----EEV 179  
  
Qy 826 GGVLELFPINGSSVVEREDVPAHLVKDIRNYFQVSPEYFSMLLVGKDGNVKSWYSPMWS 885  
|||||  
Db 180 GGVLELFPINGSSVVEREDVPAHLVKDIRNYFQVSPEYFSMLLVGKDGNVKSWYSPMWS 239  
  
Qy 886 MVIVYDLIDSMQLRRQEMAIQQSLGMRC 913  
|||||  
Db 240 MVIVYDLIDSMQLRRQEMAIQQSLGMRC 267

RESULT 5  
US-08-253-155A-36  
; Sequence 36, Application US/08253155A  
; Patent No. 5691147  
; GENERAL INFORMATION:  
; APPLICANT: Gyuris, Jeno  
; APPLICANT: Draetta, Giulio  
; TITLE OF INVENTION: CDK4 Binding Proteins  
; NUMBER OF SEQUENCES: 95  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LAHIVE & COCKFIELD  
; STREET: 60 State Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: ASCII(text)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/253,155A  
; FILING DATE: 02-JUN-1994  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Vincent, Matthew P.  
; REGISTRATION NUMBER: 36,709  
; REFERENCE/DOCKET NUMBER: MII-028  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 227-7400  
; TELEFAX: (617) 227-5941  
; INFORMATION FOR SEQ ID NO: 36:



```
; SEQUENCE CHARACTERISTICS:
; LENGTH: 358 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-08-253-155A-36
```

```
Query Match          13.7%; Score 682; DB 1; Length 358;
Best Local Similarity 66.7%; Pred. No. 5.1e-42;
Matches 144; Conservative 12; Mismatches 32; Indels 28; Gaps 4;
```

```
Qy 640 QQRDEYLESFCKMATRKISVITIFGFPVNNSTMKIDHFQLDNEKPMRVVDDDEDLVDQRLIS 699
      |||||
Db 6 QQRDEYLESFCK-----FGFPVNNSTMKIDHFQLDNEKPMRVVDDDEDVWDQRLIS 54

Qy 700 ELRKEYGMTYND---FFMVLTDVDLRVKQYYEVPITMKSVFDLIDTFQSRIDMEKQKK 755
      |||||:| | : : : : : |||||
Db 55 ELRKEYGLTYTDSSWCXQMWIXESSNTMRYQXQXSLCL---HLIDTFQSRIDMEKQKK 110

Qy 756 EGIVCKEDKKQSLNFLSRFRWRRRLLVISAPNDEDWAYSQQLSALSGQACNGLRHITI 815
      |||||
Db 111 EGIVCKEDKKQSLNFLSRFRWRRRLLVISAPNDEDWAYSQQLSALSGQACNGLRHITI 170

Qy 816 LKLLGVGEEVG-----GVLELFPINGSSVVER 842
      ||| : :| | | : ||
Db 171 LKLXALERKLGESXNCSQLMGALLLSEKTXQPICER 206
```

#### SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	212.5	4.3	1507	2	B47328	natural killer cel
2	211	4.2	2022	2	T48818	glucan 1,4-alpha-g
3	211	4.2	5327	2	T13564	microtubule-associ
4	210	4.2	1263	2	T15496	hypothetical prote
5	209.5	4.2	1618	2	S21424	nestin - human
6	209	4.2	891	2	G84693	probable proline-r
7	207.5	4.2	3488	2	T34418	hypothetical prote
8	203	4.1	706	2	A45990	junctional sarcopl
9	202	4.1	6642	2	T29757	protein UNC-89 - C
10	201.5	4.1	1560	2	T42727	proliferation pote
11	200	4.0	611	2	T22456	hypothetical prote
12	199.5	4.0	892	2	T50985	related to transcr
13	198	4.0	990	2	I51618	nucleolar phosphop
14	197.5	4.0	2526	2	T20531	hypothetical prote
15	197.5	4.0	2722	2	T20532	hypothetical prote
16	197.5	4.0	2738	2	E88320	protein F07A11.6 [
17	196.5	4.0	476	2	T27051	hypothetical prote
18	196	3.9	946	2	F88196	protein ZK1127.9 [
19	196	3.9	1015	2	JC6552	DNA topoisomerase
20	196	3.9	1087	1	QFMSH	neurofilament trip
21	193	3.9	2441	2	S39161	CREB-binding prote

#### SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2342	47.2	507	11	Q9CT39	Q9ct39 mus musculu
2	2337	47.1	867	13	Q90X49	Q90x49 brachydanio
3	1466	29.5	385	11	Q9JKW4	Q9jkw4 rattus norv
4	1148.5	23.1	358	11	Q9CRM1	Q9crml mus musculu
5	1065	21.4	209	11	Q9D6Z4	Q9d6z4 mus musculu
6	255.5	5.1	897	11	O70495	O70495 mus musculu

7	228.5	4.6	820	4	O60585	O60585 homo sapien
8	211	4.2	2090	3	Q9P6X4	Q9p6x4 neurospora
9	211	4.2	5327	5	O76891	O76891 drosophila
10	210	4.2	1422	6	Q95KU4	Q95ku4 canis famil
11	209	4.2	891	10	Q9ZW08	Q9zw08 arabidopsis
12	209	4.2	894	10	Q9FYB2	Q9fyb2 arabidopsis
13	208	4.2	1289	5	Q9VWC0	Q9vwc0 drosophila
14	205.5	4.1	3484	5	P91257	P91257 caenorhabdi
15	204.5	4.1	2951	5	Q9W3Z0	Q9w3z0 drosophila

SEQ ID NO: 26

# SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	2892.6	70.3	2927	6	AX013703	AX013703 Sequence
2	2390.4	58.1	215719	9	AC048334	AC048334 Homo sapi
3	2344.2	56.9	4467	6	AX073687	AX073687 Sequence
4	2250.6	54.7	3719	10	AF223677	AF223677 Rattus no
c 5	1830.6	44.5	168079	2	AC024709	AC024709 Homo sapi
6	1682.2	40.9	1740	6	AX073686	AX073686 Sequence
c 7	998.2	24.2	1061	6	AX188264	AX188264 Sequence
8	890	21.6	1075	6	I76208	I76208 Sequence 12
9	863	21.0	1088	6	AR020615	AR020615 Sequence
10	863	21.0	1088	6	AR044086	AR044086 Sequence
11	863	21.0	1088	6	AR085161	AR085161 Sequence
c 12	666.4	16.2	175135	2	AC079211	AC079211 Homo sapi
c 13	666.4	16.2	185101	2	AC079202	AC079202 Homo sapi
14	618.8	15.0	780	6	AX053275	AX053275 Sequence
15	263	6.4	121086	5	AL590146	AL590146 Zebrafish
c 16	227.6	5.5	250	11	G11501	G11501 SHGC-14633
17	166.8	4.1	231	6	AX186301	AX186301 Sequence
18	156.8	3.8	221	6	AX184638	AX184638 Sequence
19	153.4	3.7	168079	2	AC024709	AC024709 Homo sapi
20	151.4	3.7	182	6	AX187502	AX187502 Sequence
21	140.2	3.4	185	6	AX182067	AX182067 Sequence
c 22	113.2	2.7	790	6	AX053276	AX053276 Sequence
c 23	94.6	2.3	7218	6	I66494	I66494 Sequence 14
c 24	89.4	2.2	306	6	I76229	I76229 Sequence 57
c 25	86.4	2.1	118632	9	AL133380	AL133380 Human DNA

RESULT 8  
I76208  
LOCUS I76208 1075 bp DNA linear PAT 03-APR-1998  
DEFINITION Sequence 12 from patent US 5691147.  
ACCESSION I76208  
VERSION I76208.1 GI:3012362  
KEYWORDS .  
SOURCE Unknown.  
ORGANISM Unknown.  
Unclassified.  
REFERENCE 1 (bases 1 to 1075)  
AUTHORS Draetta,G. and Gyuris,J.  
TITLE CDK4 binding assay  
JOURNAL Patent: US 5691147-A 12 25-NOV-1997;  
FEATURES Location/Qualifiers  
source 1..1075  
/organism="unknown"  
BASE COUNT 291 a 234 c 269 g 280 t 1 others  
ORIGIN

Query Match 21.6%; Score 890; DB 6; Length 1075;  
Best Local Similarity 96.2%; Pred. No. 2.4e-193;  
Matches 975; Conservative 1; Mismatches 31; Indels 7; Gaps 6;

Qy	2918	tccacatcttcggccctgtcaacaacagcaccatgaaaatcgaccacttttcagctagata	2977
Db	44	TC TGCAAGTTCGGCCCTGTCAACAACAGCACCATGAAAATCGACCAC TTT CAGCTAGATA	103
Qy	2978	atgagaagcccatgcgagtggtgatgaagacttgtagaccagcgtctcatcagcg	3037
Db	104	ATGAGAAGCCCATGCGAGTGGTGGATGATGAAGACTGGGTAGACCAGCGTCTCATCAGCG	163
Qy	3038	agctgaggaaagagtacggaatgacctacaatgacttcttcagtggtgctaacagatgtgg	3097
Db	164	AGCTGAGGAAGGAGTACGGATTGACCTACACTGA-TTCTTCATGGTGCTAACAGATGTGG	222
Qy	3098	atctgagagtcaagcaatactatgaggtaccaataacaatgaagtctgtgtttg-atctg	3156
Db	223	ATCTGAGAGTCAAGCAATACTATGAGGTACCAATAACAATGAAGTCTGTGTTTGCACTCG	282
Qy	3157	atcgatactttccagtcgccgaatcaaagatatggagaagcagaagaaggagggcattgtt	3216
Db	283	ATCGATACTTTCCAGTCCCGAATCAAAGATATGGAGAAGCAGAAGAAGGAGGGCATTGTT	342
Qy	3217	tgcaaagaggacaaaaagcagtccttgagaaacttccatccagggttccggtggaggagg	3276
Db	343	TGCAAAGAGGACAAAAAGCAGTCCCTGGAGAACTTCCTATCCAGGTTCCGGTGGAGGAGG	402
Qy	3277	aggttgctggtgatctctgctcctaacgatgaagactgggcctattcacagcagctctct	3336
Db	403	AGGTTGCTGGTGATCTCTGCTCCTAACGATGAAGACTGGGCCTATTACAGCAGCTCTCT	462
Qy	3337	gcctcagtggtcaggcgtgcaattttggtctgcgccacataaccattctgaagctttta	3396
Db	463	GCCCTCAGTGGTCAGGCGTGCAATTGGGTCTGCGCCACATAACCATTCTGAAGC-TTTA	521
Qy	3397	ggcgttggagaggaagtgggggagtggttagaactgttcccaattaatgggagctctgtt	3456
Db	522	GGCGTTGGAGAGGAAGTTGGGGGAGTCTTAGAACTGTTCCCAATTAATGGGAGCTCTGTT	581
Qy	3457	gttgagcgagaagacgtaccagccatttggtgaagacattcgtaaactattttcaagtg	3516
Db	582	GTTGAGCGAGAAGACGTWCCAGCCCA TTT -GTGAAAGACATTCTGAACTATTTTCAAGTG	640
Qy	3517	agcccgagtgacttctccatgcttctagtcggaaaagacggaaatgtcaaatcctgggat	3576
Db	641	AGCCCGGAGTACTTCTCCATGCTTCTAGTCGGAAAAGACGGAAATGTCAAATCCTGGTAT	700
Qy	3577	ccttccccaatgtggtccatggtgattgtgtacgatttaattgattcgatgcaacttcgg	3636
Db	701	CCTTCCCAATGTGGTCCATGGTGATTGTGTACGATTTAATTGATTGATGCAACTTCGG	760
Qy	3637	agacaggaaatggcgattcagcagtcactggggatgcgctgccagaagatgagtatgca	3696
Db	761	AGACAGGAAATGGCGATT CAGCAGTCACTGGGGATGCGCTGCCAGAAGATGAGTATGCA	820
Qy	3697	ggctatggttaccatagttaccaccaaggataaccaggatgggttaccaggatgactaccgt	3756
Db	821	GGCTATGGTTACCATAGTTACCACCAAGGATACCAGGATGGTTACCAGGATGACTACCGT	880
Qy	3757	catcatgagagttatcaccatggatacccttactgagcagaaatatgtaaccttagactc	3816
Db	881	CATCATGAGAGTTATCACCATGGATACCCTTACTGAGCAGAAATATGTAACCTTAGACTC	940
Qy	3817	agccagtttctctgcagctgctaaaaactacatgtggccagctccattcttccacact-g	3875
Db	941	A--CCATTTCTCTGCAGCTGTCTGGAAC TACGATTGGCCAGCTCCATTCTTCACACTGG	998
Qy	3876	cgtactacatttctctgcctttttcttttcagtggttttttctaagactaaataaata	3929
Db	999	GGTACTACATTTCTTGCTTTTCTTTTCAAGGGTTTCTTTTAGGACTTAAATA	1052

## SUMMARIES

Result	% Query					ID	Description
	No.	Score	Match	Length	DB		
	1	4117	100.0	4117	20	AAZ09839	Human membrane spa
	2	2892.6	70.3	2927	20	AAZ42150	Human normal bladd
	3	2344.2	56.9	4467	22	AAC85085	Atherosclerosis-as
	4	1817.2	44.1	1847	22	AAH19187	Human secreted pro
	5	1757.2	42.7	1815	22	AAK94552	Human full-length
	6	1682.2	40.9	1740	22	AAC85084	Atherosclerosis-as
	7	1656.8	40.2	1792	22	AAF72810	Secreted protein g
	8	1572.2	38.2	1673	22	AAF72835	Secreted protein g
	9	1535	37.3	1561	21	AAC77711	Human cancer assoc
c	10	1512.2	36.7	1578	22	AAL36188	Human musculoskele
	11	1399.6	34.0	1438	22	AAH19228	Human secreted pro
	12	1183.8	28.8	1285	17	AAT12173	Partial pJG4-5-CDK
	13	1183.8	28.8	1285	17	AAT12174	Partial pJG4-5-CDK
c	14	998.2	24.2	1061	22	AAL26622	Human breast cance
c	15	998.2	24.2	1061	22	AAL26732	Human breast cance
c	16	998.2	24.2	1061	22	AAH72682	Human cervical can

RESULT 12

AAT12173

ID AAT12173 standard; cDNA; 1285 BP.

XX

AC AAT12173;

XX

DT 08-AUG-1996 (first entry)

XX

DE Partial pJG4-5-CDK-BP cDNA clone #125 encoding CDK4 binding protein.

XX

KW Cell cycle; regulation; G1 phase; proliferation; tumourigenesis;

KW cyclin dependent kinase; differentiation; CDK4 inhibitor; agonist;

KW antagonist; ss.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT CDS 8..845

FT /\*tag= a

FT /note= "does not contain start codon"

XX

PN WO9533819-A2.

XX

PD 14-DEC-1995.

XX

PF 02-JUN-1995; 95WO-US07113.

XX

PR 02-JUN-1994; 94US-0253155.

XX

PA (MITO-) MITOTIX INC.

XX

PI Draetta G, Gyuris J;

XX

DR WPI; 1996-040227/04.

DR

P-PSDB; AAR90544.

XX

PT Cyclin-dependent kinase-4 binding protein - used in the isolation of

PT (ant)agonists of cell cycle regulation.

XX

PS Claim 30; Page 60-61; 115pp; English.

XX

CC AAT12162-T12184 are cDNA clones of the plasmid pJG4-5-CDK-BP, or  
 CC fragments of the clones. The clones encode cyclin dependent kinase 4  
 CC (CDK4) binding proteins (CDK4-BP), which may be used in an assay for  
 CC screening test compounds as inhibitors of CDK/CDK4-BP interaction.  
 CC The complexes formed by CDK4 and D-type cyclins are strongly implicated  
 CC in the control of the early G1 phase of the cell cycle and are strong



```

      || | |||||||
Db      836 acatccgtaactatttcaagtgagcccgagtagtacttctccatgcttctagtcggaaga 895
Qy      3555 cggaaatgtcaaatcctggatccttccccaatgtggccatgggtgattgtgtacgattt 3614
      |||||||
Db      896 cggaaatgtcaaatcctggatccttccccaatgtggccatgggtgattgtgtacgattt 955
Qy      3615 aattgattcgatgcaacttcggagacaggaaatggcgattcagcagtcactggggatgcg 3674
      |||||||
Db      956 aattgattcgatgcaacttcggagacaggaaatggcgattcagcagtcactggggatgcg 1015
Qy      3675 ctgcccagaagatgagtatgcaggctatggttaccatagttaccaccaaggataccagga 3734
      |||||||
Db      1016 ctgcccagaagatgagtatgcaggctatggttaccatagttaccaccaaggataccagga 1075
Qy      3735 tggttaccaggatgactaccgtcatcatgagagttatcaccatggatacccttactgagc 3794
      |||||||
Db      1076 tggttaccaggatgactaccgtcatcatgagagttatcaccatggatacccttactgagc 1135
Qy      3795 agaaatatgtaaccttagactcagccagtttctctgcagctgctaaaactacatgtggc 3854
      |||||||
Db      1136 agaaatatgtaaccttagactcagccagtttctctgcagctgctaaaactacatgtggc 1195
Qy      3855 cagctccattcttccacactgcgtactacatttctgcctttttctttcagtggtttttct 3914
      |||||||
Db      1196 cagctccattcttccacactgcgtactacatttctgcctttttctttcagtggtttttct 1255
Qy      3915 aagactaaataaatagcaaactttcacct 3943
      |||||||
Db      1256 aagactaaataaatagcaaactttcacct 1284

```

RESULT 13

AAT12174

ID AAT12174 standard; cDNA; 1285 BP.

XX

AC AAT12174;

XX

DT 08-AUG-1996 (first entry)

XX

DE Partial pJG4-5-CDK-BP cDNA clone #127 encoding CDK4 binding protein.

XX

KW Cell cycle; regulation; G1 phase; proliferation; tumourigenesis;

KW cyclin dependent kinase; differentiation; CDK4 inhibitor; agonist;

KW antagonist; ss.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT CDS 16..894

FT /\*tag= a

FT /note= "does not contain start codon"

XX

PN W09533819-A2.

XX

PD 14-DEC-1995.

XX

PF 02-JUN-1995; 95WO-US07113.

XX

PR 02-JUN-1994; 94US-0253155.

XX

PA (MITO-) MITOTIX INC.

XX

PI Draetta G, Gyuris J;

XX

DR WPI; 1996-040227/04.

DR

P-PSDB; AAR90545.

XX

PT Cyclin-dependent kinase-4 binding protein - used in the isolation of

PT (ant)agonists of cell cycle regulation.



Qy 3375 cataaccattctgaagcttttaggcgttgagaggaagttgggggagtgttagaactgtt 3434  
 |||||  
 Db 716 cataaccattctgaagcttttaggcgttgagaggaagttgggggagtgttagaactgtt 775

Qy 3435 cccaattaatgggagctctgttgttgagcgagaagacgtaccagccatttgggtgaaaga 3494  
 |||||  
 Db 776 cccaattaatgggagctctgttgttgagcgagaagacgtaccagccatttgggtgaaag 835

Qy 3495 cattcgtaactattttcaagtgaagccggagtacttctccatgcttctagtcggaaga 3554  
 |||||  
 Db 836 acatccgtaactatttcaagtgaagccggagtacttctccatgcttctagtcggaaga 895

Qy 3555 cggaatgtcaaactcctggatccttcccaatgtggtccatgggtgattgtgtacgattt 3614  
 |||||  
 Db 896 cggaatgtcaaactcctggatccttcccaatgtggtccatgggtgattgtgtacgattt 955

Qy 3615 aattgattcgatgcaacttcggagacaggaaatggcgattcagcagtcactggggatgcg 3674  
 |||||  
 Db 956 aattgattcgatgcaacttcggagacaggaaatggcgattcagcagtcactggggatgcg 1015

Qy 3675 ctgcccagaagatgagtatgcaggctatggttaccatagttaccaccaaggataaccagga 3734  
 |||||  
 Db 1016 ctgcccagaagatgagtatgcaggctatggttaccatagttaccaccaaggataaccagga 1075

Qy 3735 tggttaccaggatgactaccgtcatcatgagagttatcacatggataacccttactgagc 3794  
 |||||  
 Db 1076 tggttaccaggatgactaccgtcatcatgagagttatcacatggataacccttactgagc 1135

Qy 3795 agaaatatgtaaccttagactcagccagtttctctgcagctgctaaaactacatgtggc 3854  
 |||||  
 Db 1136 agaaatatgtaaccttagactcagccagtttctctgcagctgctaaaactacatgtggc 1195

Qy 3855 cagctccattcttccacactgcgtactacatttctgcctttttctttcagtggttttct 3914  
 |||||  
 Db 1196 cagctccattcttccacactgcgtactacatttctgcctttttctttcagtggttttct 1255

Qy 3915 aagactaaataaatagcaaactttcacct 3943  
 |||||  
 Db 1256 aagactaaataaatagccaactttcacct 1284

Issued:

# SUMMARIES

Result	Query						Description
No.	Score	Match	Length	DB	ID		
1	890	21.6	1075	1	US-08-253-155A-12		Sequence 12, Appl
2	863	21.0	1088	1	US-08-726-525-3		Sequence 3, Appli
3	863	21.0	1088	1	US-08-487-942-3		Sequence 3, Appli
4	863	21.0	1088	2	US-08-726-036A-3		Sequence 3, Appli
5	863	21.0	1088	4	US-09-083-516-3		Sequence 3, Appli
c 6	94.6	2.3	7218	1	US-08-232-463-14		Sequence 14, Appl
c 7	89.4	2.2	306	1	US-08-253-155A-57		Sequence 57, Appl
c 8	69.4	1.7	16442	3	US-08-781-891-208		Sequence 208, App
9	68.2	1.7	2223	1	US-08-257-073-4		Sequence 4, Appli
10	61	1.5	43795	3	US-08-742-185-101		Sequence 101, App
11	57.8	1.4	240	1	US-08-628-417-6		Sequence 6, Appli
12	56.6	1.4	2447	2	US-09-014-969-14		Sequence 14, Appl
13	55.6	1.4	376	2	US-08-623-906A-18		Sequence 18, Appl
14	55.4	1.3	696	4	US-09-461-697-193		Sequence 193, App
15	55.4	1.3	699	4	US-09-461-697-191		Sequence 191, App
16	55.4	1.3	717	4	US-09-461-697-189		Sequence 189, App
17	55.4	1.3	774	4	US-09-461-697-187		Sequence 187, App
18	55.4	1.3	819	4	US-09-461-697-185		Sequence 185, App
19	55.4	1.3	1669	4	US-09-461-697-184		Sequence 184, App
20	55.2	1.3	72604	4	US-09-268-992-7		Sequence 7, Appli



```

1
US-08-253-155A-12
; Sequence 12, Application US/08253155A
; Patent No. 5691147
; GENERAL INFORMATION:
;   APPLICANT: Gyuris, Jeno
;   APPLICANT: Draetta, Giulio
;   TITLE OF INVENTION: CDK4 Binding Proteins
;   NUMBER OF SEQUENCES: 95
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: LAHIVE & COCKFIELD
;     STREET: 60 State Street
;     CITY: Boston
;     STATE: MA
;     COUNTRY: USA
;     ZIP: 02109
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: ASCII(text)
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/08/253,155A
;     FILING DATE: 02-JUN-1994
;     CLASSIFICATION: 435
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Vincent, Matthew P.
;     REGISTRATION NUMBER: 36,709
;     REFERENCE/DOCKET NUMBER: MII-028
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: (617) 227-7400
;     TELEFAX: (617) 227-5941
;   INFORMATION FOR SEQ ID NO: 12:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH: 1075 base pairs
;       TYPE: nucleic acid
;       STRANDEDNESS: single
;       TOPOLOGY: linear
;     MOLECULE TYPE: cDNA
US-08-253-155A-12

```

```

Db      403  |||||AGGTTGCTGGTGATCTCTGCTCCTAACGATGAAGACTGGGCCTATTACAGCAGCTCTCT 462
Qy      3337 gccctcagtggtcaggcgtgcaatttttggtctgcgccacataaccattctgaagctttta 3396
Db      463  |||||GCCCTCAGTGGTCAGGCGTGCAATTTGGGTCTGCGCCACATAACCATTCTGAAGC-TTTA 521
Qy      3397 ggcgttgaggaggaagtgggggagtggttagaactgttcccaattaatgggagctctgtt 3456
Db      522  |||||GGCGTTGGAGAGGAAGTTGGGGGAGTCTTAGAACTGTTCCCAATTAATGGGAGCTCTGTT 581
Qy      3457 gttgagcgagaagacgtaccagcccatttggtgaaagacattcgtaactattttcaagtg 3516
Db      582  |||||GTTGAGCGAGAAGACGTWCCAGCCCATTT-GTGAAAGACATTCGTAATATTTCAAGTG 640
Qy      3517 agcccgagtgacttctccatgcttctagtgcgaaaagacggaaatgtcaaatcctggtat 3576
Db      641  |||||AGCCCGGAGTACTTCTCCATGCTTCTAGTCGAAAAGACGGAAATGTCAAATCCTGGTAT 700
Qy      3577 ccttccccaatgtggtccatggtgattgtgtacgatttaattgattcgatgcaacttcgg 3636
Db      701  |||||CCTTCCCAATGTGGTCCATGGTGATTGTGTACGATTTAATTGATTTCGATGCAACTTCGG 760
Qy      3637 agacaggaaatggcgattcagcagtcactggggatgcgctgcccagaagatgagtatgca 3696
Db      761  |||||AGACAGGAAATGGCGATTACAGCAGTCACTGGGGATGCGCTGCCAGAAGATGAGTATGCA 820
Qy      3697 ggctatgggtaccatagttaccaccaaggataaccaggatgggtaccaggatgactaccgt 3756
Db      821  |||||GGCTATGGTTACCATAGTTACCACCAAGGATACCAGGATGGTTACCAGGATGACTACCGT 880
Qy      3757 catcatgagagttatcaccatggatacccttactgagcagaaatatgtaaccttagactc 3816
Db      881  |||||CATCATGAGAGTTATCACCATGGATACCTTACTGAGCAGAAATATGTAACCTTAGACTC 940
Qy      3817 agccagtttctctgcagctgctaaaaactacatgtggccagctccattcttccacact-g 3875
Db      941  |||||A--CCATTTCTCTGCAGCTGTGGAACACGATTGGCCAGCTCCATTCTTCACACTGG 998
Qy      3876 cgtactacatttctgcctttttctttcagtgtttttctaagactaaataaata 3929
Db      999  |||||GGTACTACATTCTGGCTTTTCTTTCAAGGGTTTTTCTTTAGGACTTAAATA 1052

```

RESULT 2

US-08-726-525-3

; Sequence 3, Application US/08726525

; Patent No. 5789181

; GENERAL INFORMATION:

; APPLICANT: Lin, Lih-Ling

; APPLICANT: Graham, James

; TITLE OF INVENTION: NOVEL INTERLEUKIN-1 RECEPTOR

; TITLE OF INVENTION: INTRACELLULAR LIGAND PROTEINS AND INHIBITORS OF LIGAND

; TITLE OF INVENTION: BINDING

; NUMBER OF SEQUENCES: 7

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: LEGAL AFFAIRS, GENETICS INSTITUTE, INC.

; STREET: 87 CambridgePark Drive

; CITY: Cambridge

; STATE: MA

; COUNTRY: USA

; ZIP: 02140

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/726,525

; FILING DATE: 07-OCT-1996

; CLASSIFICATION: 435

```

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/487,942
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; REFERENCE/DOCKET NUMBER: GI5258
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1088 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 2..961
US-08-726-525-3

```

Query Match 21.0%; Score 863; DB 1; Length 1088;  
Best Local Similarity 85.3%; Pred. No. 6.9e-230;  
Matches 1067; Conservative 0; Mismatches 0; Indels 184; Gaps 2;

Qy	2694	gaaaaaaggagggtaaaacagaacaggatggctatcagaaacccaccaacaacacttcac	2753
Db	1	GAAAAAAGGAGGTTAAACAGAACAGGATGGCTATCAGAAACCCACCAACAAACACTTCAC	60
Qy	2754	gcagagtgcccaagaagtgcagtgccgacctgctggggctcctttgaaggcaaacgaagact	2813
Db	61	GCAGAGTCCCAAGAAGTCAGTGGCCGACCTGCTGGGGTCCTTTGAAGGCAAACGAAGACT	120
Qy	2814	ccttctgatcactgctcccaaggctgagaacaatatgtatgtgcaacaacgtgatgaata	2873
Db	121	CCTTCTGATCACTGCTCCCAAGGCTGAGAACAAATATGTATGTGCAACAACGTGATGAATA	180
Qy	2874	tctggaaagtttctgcaagatggctaccaggaaaaatctctgtgatcaccatcttcggccc	2933
Db	181	TCTGGAAAGTTTCTGCAAGATGGCTACCAGGAAAATCTCTGTGATCACCATCTTCGGCCC	240
Qy	2934	tgtcaacaacagcaccatgaaaatcgaccactttcagctagataatgagaagcccatgcg	2993
Db	241	TGTCAACAACAGCACCATGAAAATCGACCACTTTCAGCTAGATAATGAGAAGCCCATGCG	300
Qy	2994	agtgggtgatgatgaagacttggtagaccagcgtctcatcagcgagctgaggaaagagta	3053
Db	301	AGTGGTGGATGATGAAGACTTGGTAGACCAGCGTCTCATCAGCGAGCTGAGGAAAGAGTA	360
Qy	3054	cggaatgacctacaatgacttcttcattggtgctaacagatgtggatctgagagtcaagca	3113
Db	361	CGGAATGACCTACAATGACTTCTTCATGGTGCTAACAGATGTGGATCTGAGAGTCAAGCA	420
Qy	3114	atactatgaggtaccaataacaatgaagctctgtgtttgatctgatcgatactttccagtc	3173
Db	421	ATACTATGAGGTACCAATAACAATGAAGTCTGTGTTTGATCTGATCGATACTTCCAGTC	480
Qy	3174	ccgaatcaagatatggagaagcagaagaaggagggcattgtttgcaagaggacaaaaa	3233
Db	481	CCGAATCAAAGATATGGAGAAGCAGAAGAAGGAGGGCATTGTTTGCAA-----	528
Qy	3234	gcagtcctctggagaacttcctatccaggttcgggtggaggaggaggttgctggtgatctc	3293
Db	529	-----	528
Qy	3294	tgctcctaacgatgaagactgggcctattcacagcagctctctgcctcagtggtcaggc	3353
Db	529	-----	528

Qy 3354 gtgcaattttggtctgcgccacataaccattctgaagcttttaggcgttgagaggaagt 3413  
 Db 529 -----AGAGGAAGT 537

Qy 3414 tgggggagtggttagaactgttcccaattaatgggagctctgttggtagcgagaagacgt 3473  
 Db 538 TGGGGGAGTGTTAGAACTGTTCCCAATTAATGGGAGCTCTGTTGTTGAGCGAGAAGACGT 597

Qy 3474 accagcccatttgggtgaaagacattcgttaactattttcaagtgagcccgagtagtcttc 3533  
 Db 598 ACCAGCCCATTGTTGGTGAAAGACATTCGTAACATTTTCAAGTGAGCCCGAGTACTTCTC 657

Qy 3534 catgcttctagtcggaaaagacggaaatgtcaaatcctggatccttccccaatgtggtc 3593  
 Db 658 CATGCTTCTAGTCGGAAAAGACGGAAATGTCAAATCCTGGTATCCTTCCCCAATGTGGTC 717

Qy 3594 catgggtattgtgtacgatttaattgattcgatgcaacttcggagacaggaaatggcgat 3653  
 Db 718 CATGGTGATTGTGTACGATTTAATTGATTCGATGCAACTTCGGAGACAGGAAATGGCGAT 777

Qy 3654 tcagcagtcactggggatgcgctgcccagaagatgagtatgcaggctatggttaccatag 3713  
 Db 778 TCAGCAGTCACTGGGGATGCGCTG-CCAGAAGATGAGTATGCAGGCTATGGTTACCATAG 836

Qy 3714 ttaccaccaaggataaccaggatgggtaccaggatgactaccgtcatcatgagagttatca 3773  
 Db 837 TTACCACCAAGGATACCAGGATGGTTACCAGGATGACTACCGTCATCATGAGAGTTATCA 896

Qy 3774 ccatggatacccttactgagcagaaatatgtaaccttagactcagccagtttctctgca 3833  
 Db 897 CCATGGATACCCTTACTGAGCAGAAATATGTAACCTTAGACTCAGCCAGTTTCTCTGCA 956

Qy 3834 gctgctaaaaactacatgtggccagctccattcttccacactgcgtactacatttctgccc 3893  
 Db 957 GCTGCTAAAACTACATGTGGCCAGCTCCATTCTCCACACTGCGTACTACATTCTCTGCC 1016

Qy 3894 tttttcttttcagtgttttttctaagactaaataaatagcaaaactttcaccta 3944  
 Db 1017 TTTTCTTTTCAGTGTTTTTCTAAGACTAAATAAATAGCAAACTTTCACCTA 1067

# SUMMARIES

Result	Score	Query	Match	Length	DB	ID	Description
No.							
1	1273.2	30.9	1679	11	AK011256		AK011256 Mus muscu
2	1022.4	24.8	1550	11	BC022704		BC022704 Mus muscu
3	717.8	17.4	746	10	BE889110		BE889110 601513557
4	713	17.3	886	10	BG035195		BG035195 602324702
5	709.8	17.2	902	11	AK009795		AK009795 Mus muscu
6	704.8	17.1	857	10	BI763566		BI763566 603050110
7	702.4	17.1	738	10	BM051031		BM051031 603633915
8	679.2	16.5	818	10	BG120262		BG120262 602353649
9	678.8	16.5	1199	10	BG253437		BG253437 602363350
10	671.8	16.3	1057	10	BF338364		BF338364 602034007
11	670.2	16.3	881	10	BI830199		BI830199 603072871
12	668.8	16.2	723	10	BG122685		BG122685 602351812
13	663	16.1	832	10	BI109173		BI109173 602897030
14	660.2	16.0	806	10	BI109220		BI109220 602897087
c 15	654.2	15.9	659	9	AW303375		AW303375 xv18c11.x
16	651.8	15.8	749	10	BF037455		BF037455 601461038
17	651.8	15.8	1074	11	AK020169		AK020169 Mus muscu